

RL J. BIOL. CHEM. 267:21172-21178(1992). HIGH AFFINITY FOR TNA-ALPHA AND
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-BETA.
 CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
 CC -1- PPM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
 CC LEVEL ON THREONINE RESIDUES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC EMBL: M32315; G189186; -
 DR EMBL: M35857; G339752; -
 DR EMBL: M35944; G339758; -
 DR PIR: A35356; A35356.
 DR PIR: A36007; A36007.
 DR PIR: A36475; A36475.
 DR PIR: B35010; B35010.
 DR PIR: A23666; A23666.
 DR HSP: P19438; 1TNR.
 DR MIM: 19191; -
 DR PROSITE: PS00652; TNFR_NGFR.
 DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL;
 KW PHOSPHORYLATION.
 FT SIGNAL 1 22 TUMOR NECROSIS FACTOR RECEPTOR 2.
 FT CHAIN 23 461 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 258 257 POTENTIAL.
 FT TRANSMEM 258 287 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 288 461 4 X TNFR-CYS.
 FT DOMAIN 39 201 TNFR-CYS 1.
 FT REPEAT 39 76 TNFR-CYS 2.
 FT REPEAT 77 118 TNFR-CYS 3.
 FT REPEAT 119 162 TNFR-CYS 4.
 FT REPEAT 163 201 TNFR-CYS 4.
 FT REPEAT 163 201 BY SIMILARITY.
 FT DISULFID 40 53 BY SIMILARITY.
 FT DISULFID 54 67 BY SIMILARITY.
 FT DISULFID 57 75 BY SIMILARITY.
 FT DISULFID 78 93 BY SIMILARITY.
 FT DISULFID 96 110 BY SIMILARITY.
 FT DISULFID 100 118 BY SIMILARITY.
 FT DISULFID 120 126 BY SIMILARITY.
 FT DISULFID 134 143 BY SIMILARITY.
 FT DISULFID 137 161 BY SIMILARITY.
 FT DISULFID 164 179 BY SIMILARITY.
 FT CARBOHYD 171 171 POTENTIAL.
 FT CARBOHYD 193 193 R -> P (IN REF. 3).
 FT CONFLICT 141 141 R -> M (IN REF. 1).
 FT CONFLICT 196 196 R -> T (IN REF. 3).
 FT CONFLICT 363 363 A -> T (IN REF. 3).
 FT SEQUENCE 461 AA; 48316 MW; 0F5D0C44 CRC32;
 SQ SEQUENCE 461 AA; 48316 MW; 0F5D0C44 CRC32;
 Query Match 14.2%; Score 405; DB 9; Length 461;
 Best Local Similarity 41.8%; Pred. No. 6,30e-63;
 Matches 69; Conservative 26; Mismatches 59; Indels 11; Gaps 8;

CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 9187885.
 RA LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
 RA WONG G.H., CHEN E.Y., GOEDEL D.V.,
 RA PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE; 91246168.
 RA GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
 RA COPELAND N.G., JENKINS N.A., SMITH C.A.,
 RA MOL. CELL. BIOL. 11:3020-3026(1991).
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC EMBL: M60469; G199828; -
 DR EMBL: M59378; G202095; -
 DR PIR: B38634; B38634.
 DR HSP: P19438; 1TNR.
 DR PROSITE: PS00652; TNFR_NGFR.
 DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
 KW SIGNAL 1 22 TUMOR NECROSIS FACTOR RECEPTOR 2.
 FT CHAIN 23 474 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 258 258 POTENTIAL.
 FT TRANSMEM 258 288 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 288 474 4 X TNFR-CYS.
 FT DOMAIN 39 203 TNFR-CYS 1.
 FT REPEAT 39 77 TNFR-CYS 2.
 FT REPEAT 78 119 TNFR-CYS 3.
 FT REPEAT 120 164 TNFR-CYS 4.
 FT REPEAT 165 203 TNFR-CYS 4.
 FT REPEAT 165 203 BY SIMILARITY.
 FT DISULFID 40 54 BY SIMILARITY.
 FT DISULFID 55 68 BY SIMILARITY.
 FT DISULFID 58 76 BY SIMILARITY.
 FT DISULFID 79 94 BY SIMILARITY.
 FT DISULFID 97 111 BY SIMILARITY.
 FT DISULFID 101 119 BY SIMILARITY.
 FT DISULFID 121 127 BY SIMILARITY.
 FT DISULFID 136 145 BY SIMILARITY.
 FT DISULFID 139 163 BY SIMILARITY.
 FT DISULFID 166 181 BY SIMILARITY.
 FT CARBOHYD 69 69 POTENTIAL.
 FT CARBOHYD 195 195 POTENTIAL.
 FT SEQUENCE 474 AA; 50319 MW; DC32B286 CRC32;
 SQ SEQUENCE 474 AA; 50319 MW; DC32B286 CRC32;
 Query Match 13.1%; Score 375; DB 9; Length 474;
 Best Local Similarity 41.5%; Pred. No. 3.56e-56;
 Matches 66; Conservative 21; Mismatches 61; Indels 11; Gaps 7;

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUKARYOTA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 89356608.
 RX STAMENKOVIC I., CLARK E.A., SEED B.;
 RL EMO J. 8:1403-1410(1989).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL; X60592; G29851; -
 DR PIR; S04460; S04460.
 DR MIR; 109535; -
 DR PROSITE; PS00652; TNFR_NGFR.
 KW RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 277
 FT DOMAIN 20 193
 FT TRANSMEM 194 215
 FT DOMAIN 216 277
 FT DOMAIN 25 187
 FT REPEAT 25 187
 FT REPEAT 61 103
 FT REPEAT 104 144
 FT REPEAT 145 187
 FT CARBOHYD 153 153
 FT CARBOHYD 180 180
 SQ SEQUENCE 277 AA; 30619 MW; 3B284411 CRC32;

Query Match 10.6%; Score 303; DB 2; Length 277;
 Best Local Similarity 36.8%; Pred. No. 2,64e-40;
 Matches 56; Conservative 21; Mismatches 67; Indels 8; Gaps 7;

Db 38 cdicpgqgklysdctefetecldpcgeesefldvnrchqkqydcnp-1g1r-vyqkg 95
 41 CDKCPPTLYLKQHCITAKMTKVCAPCPDHYTDSWHTSDEC-L--YCSVCKELQYVQEC 97
 Db 96 tsetdtctceegwhctseacescvlhscspgfgvqkqatgvsdltcepcvpgffnvs 155
 98 NRTNHRVCECKEGRY-L-EI-EFCLKHSRCPGFGVQAGTPERNVTCKRCPDGFFSNET 154
 Db 156 safekchpwtscetkdlvvgagqntkdvvg 187
 155 SSKAPCRKHTNCVFGLLTQKGNATHDNICS 186
 QY

RESULT 4
 AC CD40_MOUSE STANDARD; PRT; 289 AA.
 AC P27512;
 DT 01-APR-1992 (REL. 23, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
 GN CD40.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUKARYOTA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 92105763.
 RX TORRES R.M., CLARK E.A.;
 RL J. IMMUNOL. 148:620-626(1992).
 CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
 ANTI-VIRAL EFFECTS OF THE CYTOKINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL; M95181; G332310; -
 DR EMBL; A23729; E199442; -
 DR PIR; A40566; G0VZML.
 DR HSSP; P19438; ITNR.
 DR PROSITE; PS00652; TNFR_NGFR.
 KW RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.
 FT SIGNAL 1 16
 FT CHAIN 17 326
 FT DOMAIN 27 186

RA GRIMALDI J.C., TORRES R., KOZAK C.A., CHANG R., CLARK E.A.,
 RX MEDLINE; 93094586.
 RP STRAIN-BALB/C; TISSUE-LIVER;
 RC SEQUENCE FROM N.A.
 RL [3]
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
 DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
 GN T2.
 OS MYXOMA VIRUS (STRAIN LAUSANNE).
 OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXYVIRIDAE; CHOROPOXVIRINAE;
 OC LEPOPOVIRUSES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 91335768.
 RX UPTON C., MACEN J.L., SCHREIBER M., MCFADDEN G.;
 RL VIROLOGY 184:370-382(1991).
 CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
 REACH CELLULAR TARGET AND THEREBY DEAPENING THE POTENTIAL
 ANTI-VIRAL EFFECTS OF THE CYTOKINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL; M95181; G332310; -
 DR EMBL; A23729; E199442; -
 DR PIR; A40566; G0VZML.
 DR HSSP; P19438; ITNR.
 DR PROSITE; PS00652; TNFR_NGFR.
 KW RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.
 FT SIGNAL 1 16
 FT CHAIN 17 326
 FT DOMAIN 27 186

RA HOWARD M., COCKAYNE D.A.;
 RL J. IMMUNOL. 149:3921-3926(1992).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL; M83312; G1553059; -
 DR EMBL; M94126; G192526; -
 DR EMBL; M94128; G192526; JOINED.
 DR EMBL; M94128; G192526; JOINED.
 DR EMBL; M94127; G192526; JOINED.
 DR PIR; A46476; A46476.
 DR HSSP; P19438; ITNR.
 DR PROSITE; PS00652; TNFR_NGFR.
 KW RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 289
 FT DOMAIN 20 193
 FT TRANSMEM 194 215
 FT DOMAIN 216 289
 FT DOMAIN 25 187
 FT REPEAT 25 187
 FT REPEAT 61 103
 FT REPEAT 104 144
 FT REPEAT 145 187
 FT CARBOHYD 153 153
 SQ SEQUENCE 289 AA; 32111 MW; D8D70A2C CRC32;

Query Match 10.3%; Score 294; DB 2; Length 289;
 Best Local Similarity 38.8%; Pred. No. 2,31e-38;
 Matches 59; Conservative 20; Mismatches 65; Indels 8; Gaps 6;

Db 38 cdicpgsrltshctalektqchpcdsgefsaqwnreirchqhncpn-vg1r-vkkg 95
 41 CDKCPPTLYLKQHCITAKMTKVCAPCPDHYTDSWHTSDEC-LX--CSVCKELQYVQEC 97
 Db 96 taedvtctckegqchskdcacacqhtpctprgfygmemttdtctchpcpygfngs 155
 98 NRTNHRVCECKEGRY-L-EI-EFCLKHSRCPGFGVQAGTPERNVTCKRCPDGFFSNET 154
 Db 156 sflekcyptwscetkdlvvgagqntkdvvg 187
 155 SSKAPCRKHTNCVFGLLTQKGNATHDNICS 186
 QY

RESULT 5
 ID VT2_MXVVL STANDARD; PRT; 326 AA.
 AC P29825;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
 DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
 GN T2.
 OS MYXOMA VIRUS (STRAIN LAUSANNE).
 OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXYVIRIDAE; CHOROPOXVIRINAE;
 OC LEPOPOVIRUSES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 91335768.
 RX UPTON C., MACEN J.L., SCHREIBER M., MCFADDEN G.;
 RL VIROLOGY 184:370-382(1991).
 CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
 REACH CELLULAR TARGET AND THEREBY DEAPENING THE POTENTIAL
 ANTI-VIRAL EFFECTS OF THE CYTOKINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL; M95181; G332310; -
 DR EMBL; A23729; E199442; -
 DR PIR; A40566; G0VZML.
 DR HSSP; P19438; ITNR.
 DR PROSITE; PS00652; TNFR_NGFR.
 KW RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.
 FT SIGNAL 1 16
 FT CHAIN 17 326
 FT DOMAIN 27 186

Query Match	Similarity	Score	DB %	Length
Best Local	54; Conservative	28.9%	Pred. No. 3,52e-32;	Indels 11; Gaps 8;
Matches	54; Conservative	30; Mismatches	92; Indels	11; Gaps
52	emphayccscppgefavcsrgdvtcktpchmsynehnhlstqqlcrp-cdiylgfi110			
Db	111	eevqetstskkccrcqpgmcsvylidnacvchceerilvcpgtaeavtdeimgtdvncv170		
Qy	93	vr-qecnrtrhnrvckckesr---yleie-fclknrr-s-cpfggfv-yoagtperrntvck143		
Db	171	pekpghfgntsparcqphtrcicqigjaveaagpysdcltkpppepamllajlisl230		
Qy	144	rcpddgfssmetskacrkrrhncsvfgliltokgnatdhncsgnsstokcgcivtlce203		
Db	231	viflilt237		
Qy	204	EAFFFA210		
RESULT				
ID	VF2_SFVKA	STANDARD;	PRT;	325 AA.
AC	P25943;			
DT	01-MAY-1992 (REL. 22, CREATED)			
DT	01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)			
DT	01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)			
DE	TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).			
GN	T2.			
OS	SHOPE FIBROMA VIRUS (STRAIN KASZA) (SEV).			
OC	VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;			
OC	LEPORIPOVIRUSES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 87321103.			
RA	UPTON C., DELANGE A.M., MCFADDEN G.;			
RL	VIROLOGY 160:20-30(1987).			
RN	[2]			
RP	FUNCTION.			
RX	MEDLINE; 91207415.			
RA	SMITH C.A., DAVIS T., WIGNALL J.M., DIN W.S., FARRAH T., UPTON C.,			
RL	MCRADDEN G., GOODWIN R.G.;			
CC	BIOCHEM. BIOPHYS. RES. COMMUN. 176:335-342(1991).			
CC	-I- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO			
CC	REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL			
CC	ANTIVIRAL EFFECTS OF THE CYTOKINE.			
CC	-I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
CC	EMBL; M17433; -; NOT ANNOTATED_CDS.			
DR	EMBL; A23727; E199408; -.			
DR	PIR; B43692; B43692.			
DR	HSSP; P19458; 11NR.			
DR	DR PROSITE; PS00652; TNFR_NGFR.			
KW	RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.			
FT	SIGNAL	1	16	POTENTIAL.
FT	CHAIN	17	325	PROTEIN T2.
FT	DOMAIN	27	186	4 X TNFR-CYS.
FT	REPEAT	27	62	TNFR-CYS 1.
FT	REPEAT	105	104	TNFR-CYS 2.
FT	REPEAT	105	147	TNFR-CYS 3.
FT	REPEAT	148	186	TNFR-CYS 4.
FT	CARBOHYD	105	105	POTENTIAL.
FT	CARBOHYD	105	181	POTENTIAL.
FT	CARBOHYD	205	205	POTENTIAL.
FT	CARBOHYD	238	238	POTENTIAL.

SQ SEQUENCE 325 AA; 35132 MW; C9D2C87B CRC32;
Query Match 9.1%; Score 260; DB 10; Length 325;
Best Local Similarity 30.5%; Pred. No. 3,98e-31;
Matches 51; Conservative 31; Mismatches 77; Indels 8; Gaps 5;
Db 40 caschgfysaricgpgsnvscpscedgttastahapacvscrgpctghlssgpcodrt 99
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 41 CDCPCPGTYLKQHCCTAKWKIVCAPCPDHYTDSMTSDCLVCSPLYCKELQYVKQECNRT 100
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 100 hdtvncstnycllygqngcrlicapqtkcpaggyvs-ghttagdclcekcphlydsdl 158
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 101 HNHVCECKEGRY--L--EID--FCLKHRSCLPFGVVOAGTPEPRTVCKRCPCDGFSGNET 154
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 159 speregrtsfnysvgnlypvnetsctt-aghneviktketfvcl 204
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 155 SSKAPCKRHTNCSVFGLLTQKGNATHDNICSGNSESTORCGIDVTL 201
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
RESULT 8
TNR_C_HUMAN STANDARD; PRT; 435 AA.
AC P36941;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
GN TNFR.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RC MEDLINE: 93252381.
RA BAENS M., CHAFFANET M., CASSIMAN J.J., DEN BERGHE H., MARINEN P.;
RL GENOMICS 16:214-218(1993).
RN [2]
RP FUNCTION: 94225209.
RA CROWE P.D., VAN ARSDALE T.L., WALTER B.N., WARE C.F., HESSON C.,
REHRENFELS B., BROWNING J.L., DIN W.S., GOODWIN R.G., SMITH C.A.;
RL SCIENCE 264:707-710(1994).
CC -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
IMMUNE DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL: L04270; G339762; -
MTM: 600979; -
HSSP: P19999; ICLG.
DR PROSITE: PS00652; TNFR_NGFR.
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
FT SIGNAL. 1 30
FT CHAIN 31 435
FT DOMAIN 227 227
FT TRANSMEM 228 248
FT DOMAIN 249 435
FT DOMAIN 42 211
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 168
FT REPEAT 169 211
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 148
FT DISULFID 142 167
FT DISULFID 170 185
FT CARBOHYD 40 40
POTENTIAL.

FT CARBOHYD 177 177
SQ SEQUENCE 435 AA; 46709 MW; 203B82DD CRC32; POTENTIAL.
Query Match 9.1%; Score 260; DB 9; Length 435;
Best Local Similarity 32.3%; Pred. No. 3,98e-31;
Matches 52; Conservative 23; Mismatches 75; Indels 11; Gaps 6;
Db 52 ephrlicscrcppgytvasakcsirtdtcatcaensynehmylltclqclrcpdcy-tmgl 110
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 34 ETSHQLCDKCPGTYLKQHCCTAKWKIVCAPCPDHYTDSMTSDCLV--CSPYCKEL 90
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 111 eelap-ctskrktrcgqgmfcawalecthccllisdcppteaelkdevgkgnhcyrp 169
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 91 QYVKQECNRTNHNVCCECKEGRY-----LEIFCLKHRSCLPFGV--VOAGTPEPRTVCKR 144
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 170 ckaghqntsspaarcqphtrcenglvaeapqtsdttc 210
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 145 CPDGFSGNETSSKAPCKRHTNCSVFGLLTQKGNATHDNIC 185
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
RESULT 9
ID VC22-VARV STANDARD; PRT; 349 AA.
AC P34015;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE PROTEIN C22/B28 HOMOLOG.
GN GAR.
OS VARIDOLA VIRUS.
OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
OC ORTHOPOXVIRUSES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=INDIA-1967 / ISOLATE IND3;
RC MEDLINE: 93202281.
RA SHECHELKUNOV S.N., BLINOV V.M., SANDAKHCHIEV L.S.;
RL FEBS LETT. 319:80-83(1993).
CC -!- SIMILARITY: CONTAINS TWO LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.
EMBL: X69198; G457087; -
DR EMBL: X67117; G516449; -
DR PIR: D36858; D36858.
DR PIR: S35987; S35987.
DR PIR: S46888; S46888.
DR HSSP: P19438; ITNR.
DR PROSITE: PS00652; TNFR_NGFR.
KW REPEAT.
FT DOMAIN 31 108
FT REPEAT 31 66
FT REPEAT 67 108
FT REPEAT 108 108
SQ SEQUENCE 349 AA; 38189 MW; 50D0B435 CRC32; 2 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
TNFR-CYS 5.
TNFR-CYS 6.
TNFR-CYS 7.
TNFR-CYS 8.
TNFR-CYS 9.
TNFR-CYS 10.
TNFR-CYS 11.
TNFR-CYS 12.
TNFR-CYS 13.
TNFR-CYS 14.
TNFR-CYS 15.
TNFR-CYS 16.
TNFR-CYS 17.
TNFR-CYS 18.
TNFR-CYS 19.
TNFR-CYS 20.
TNFR-CYS 21.
TNFR-CYS 22.
TNFR-CYS 23.
TNFR-CYS 24.
TNFR-CYS 25.
TNFR-CYS 26.
TNFR-CYS 27.
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 SQ SEQUENCE 461 AA; 50969 MM; 82F68B08 CRC32;
 Query Match 7.7%; Score 220; DB 9; Length 461;
 Best Local Similarity 33.8%; Pred. No. 7.09e-23;
 Matches 49; Conservative 22; Mismatches 63; Indels 11; Gaps 10;
 Db 49 yabphnslctckhkytlysdcpypgqetvcevcckgftasqnhvrgclskctcke 108
 31 YDETSHQLLCDKCPGTYLKQCHCTAK-WKTVGAPCPDHYTDSWHTSDCLYCSPVCKE 89
 109 mfvvelspckadmtcgckngfyrlsethfcvcdscpfng-vtltpckekqntvcn 167
 90 L-QYVROECNRTNHRVCEK--E-GRTL-EIEF-CLKHRSCTPGFGVYAGTPEBNTVCK 143
 QY 168 -chagfflsnecpshckngcec 191
 144 RCPDGF-S-NEISSKAPCRKHTNC 166
 Db 168 -chagfflsnecpshckngcec 191
 144 RCPDGF-S-NEISSKAPCRKHTNC 166
 QY 168 -chagfflsnecpshckngcec 191
 144 RCPDGF-S-NEISSKAPCRKHTNC 166
 RESULT 12
 ID NGFR-CHICK STANDARD; PRT; 416 AA.
 AC P18519;
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
 DE (GP80-LINGFR).
 OS GALLUS GALLUS (CHICKEN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
 OC GALLIFORMES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE: 90166579
 RA LARGE T.H., WESEKAMP G., HELDER J.C., RADEKE M.J., MISKO T.P.,
 RA SHOOTER E.M., REICHARDT L.F.;
 RA NEURON 2:1123-1134(1989).
 [2]
 SEQUENCE OF 21-416 FROM N.A.
 KA MEDLINE: 90152140.
 RA HEUER J.G., FATEMIE-NAINE S., WHEELER E.F., BOTHWELL M.;
 RL DEV. BIOL. 137:287-304(1990).
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
 NT-3, AND NT-4.
 CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
 BOND FORMATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR PIR: J00006; J00006.
 DR PIR: A60504; A60504.
 DR PROSITE: PS00652; TNFR_NGFR.
 DR PROSITE: PS0017; DEATH_DOMAIN.
 KW RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
 KW PHOSPHORYLATION; SIGNAL.
 FT CHAIN 1 19 POTENTIAL.
 FT CHAIN 20 416 NGF RECEPTOR
 FT DOMAIN 28 239 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 240 261 POTENTIAL.
 FT DOMAIN 262 416 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 23 181 4 X TNFR-CYS.
 FT REPEAT 23 57 TNFR-CYS 1.
 FT REPEAT 56 100 TNFR-CYS 2.

FT REPEAT 101 140 TNFR-CYS 3.
 FT REPEAT 141 181 TNFR-CYS 4.
 FT DOMAIN 188 236 SER/TNR-RICH.
 FT DOMAIN 333 410 DEATH DOMAIN.
 FT DISULFID 24 35 BY SIMILARITY.
 FT DISULFID 36 49 BY SIMILARITY.
 FT DISULFID 39 56 BY SIMILARITY.
 FT DISULFID 59 75 BY SIMILARITY.
 FT DISULFID 78 91 BY SIMILARITY.
 FT DISULFID 81 99 BY SIMILARITY.
 FT DISULFID 101 114 BY SIMILARITY.
 FT DISULFID 117 130 BY SIMILARITY.
 FT DISULFID 120 138 BY SIMILARITY.
 FT DISULFID 141 156 BY SIMILARITY.
 FT DISULFID 159 172 BY SIMILARITY.
 FT DISULFID 162 180 BY SIMILARITY.
 FT CARBOHYD 52 52 POTENTIAL.
 FT CARBOHYD 36 36 C -> Y (IN REF. 2).
 FT CONFLICT 173 173 T -> K (IN REF. 2).
 FT CONFLICT 276 276 N -> S (IN REF. 2).
 FT CONFLICT 396 396 K -> R (IN REF. 2).
 SQ SEQUENCE 416 AA; 44654 MM; 4D3F086A CRC32;
 Query Match 7.5%; Score 215; DB 6; Length 416;
 Best Local Similarity 30.4%; Pred. No. 7.20e-22;
 Matches 45; Conservative 27; Mismatches 70; Indels 6; Gaps 6;
 Db 36 ckaenlgevgvpcgvn-qtvepcldsvtysdtsvatepckpctg-cvylhmsapcve 93
 41 CDKCPGTYLKQCHCTAKWTVGAPCPDHY-YTDSWHTSDCLYCSPVCKELQYKQECNR 99
 Db 94 sdavrcrcayyfgdelsckscsicevgfllmfcrcsdvceecpctgtsdaanf 153
 100 TNHRVCEKREGRTL-EIE-FCLKHRSCTPGFGVYAGTPEBNTVCKRCPDGFSENETSSK 157
 QY 154 dpcplcticeenmvwke-ctatsdaec 180
 Db 154 dpcplcticeenmvwke-ctatsdaec 180
 158 APCKRHTNCSVFELLTOKGNATHDNIC 185
 QY 158 APCKRHTNCSVFELLTOKGNATHDNIC 185
 RESULT 13
 ID NGFR-HUMAN STANDARD; PRT; 427 AA.
 AC P08138;
 DT 01-AUG-1988 (REL. 08, CREATED)
 DT 01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
 DE (GP80-LINGFR).
 GN NGFR.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87051725.
 RA JOHNSON D., LANAHAN A., BUCK C.R., SEHGAL A., MORGAN C., MERCER E.,
 RA BOTHWELL M., CHAO M.;
 RL CELL 47:545-554(1986).
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
 NT-3, AND NT-4.
 CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
 BOND FORMATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: M4764; G189205; -.
 DR PIR: A25218; GQHUN.
 DR HSP: P19438; ITNR.
 DR MIM: 162010; -.
 DR PROSITE: PS00652; TNFR_NGFR.
 DR PROSITE: PS0017; DEATH_DOMAIN.
 KW RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
 KW PHOSPHORYLATION; SIGNAL.

FT SIGNAL 1 28
 FT CHAIN 29 427
 FT DOMAIN 29 250
 FT TRANSSEM 251 272
 FT DOMAIN 273 427
 FT DOMAIN 31 189
 FT REPEAT 31 65
 FT REPEAT 66 107
 FT REPEAT 108 147
 FT REPEAT 148 189
 FT DOMAIN 344 421
 FT DISULFID 32 43
 FT DISULFID 44 57
 FT DISULFID 47 64
 FT DISULFID 67 83
 FT DISULFID 86 99
 FT DISULFID 89 107
 FT DISULFID 109 122
 FT DISULFID 125 138
 FT DISULFID 128 146
 FT DISULFID 149 164
 FT DISULFID 167 180
 FT DISULFID 170 188
 FT DISULFID 197 248
 FT DOMAIN 197 248
 FT CARBOHYD 60 60
 FT SEQUENCE 427 AA; 45183 MW; EE2924BD CRC32;

Query Match 7.48; Score 213; DB 6; Length 427;
 Best Local Similarity 34.9%; Pred. No. 1,81e-21;
 Matches 45; Conservative 19; Mismatches 60; Indels 5; Gaps 5;

DB 44 ckaclnlgvayqpgan-gtycepcldsvtfsdvsatepckpcte-cvlglsmsapve 101
 QY 41 CDKCPGGTYLKQHCATKATYCAPCPDH-YTDSWHTSDCLYCSVCKELQVYKQECNR 99
 DB 102 addavrcaygygdeetgtrceacvcsqglvifscqdkgnlycecpdgtydsdeanhv 161
 QY 100 THNRVCECKEGRYL-EI-EFLKHSRCPGGVQAGTPERNIVCKRCPDGFNSMSSK 157
 DB 162 dpcldpctvc 170
 QY 158 APCRKHNC 166

RESULT 14
 ID NGFR RAT STANDARD: PRT: 425 AA.
 AC P07174;
 01-APR-1988 (REL. 07, CREATED)
 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
 DE (GP80-LINGFR).
 GN NGFR.
 OS RATTUS NORVEGICUS (RAT).
 OS EURARCTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 CC [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 87115859.
 RX RADEKE M.J., MISKO T.P., HSU C., HERZENBERG L.A., SHOOTER E.M.;
 RA NATURE 325:593-597(1987).
 RL [2]
 RN SEQUENCE OF 1-22 FROM N.A.
 RP TISSUE-LIVER.
 RC MEDLINE: 93077038.
 RA METSIS M., TIMMUS T., ALLIKMETS R., SAARMA M., PERSSON H.;
 RL GENE 121:247-254(1992).
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
 CC -1- NT-3, AND NT-4.
 CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
 CC -1- BOND FORMATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.

CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: X05137; G56736; ...
 DR EMBL: X61269; -; NOT_ANNOTATED_CDS.
 DR PIR: A26431; A26431.
 DR HSSP: P19438; TNFR.
 DR PROSITE: P500652; TNFR_NGFR.
 DR PROSITE: P500017; DEATH_DOMAIN.
 DR RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
 KW PHOSPHORYLATION; SIGNAL.
 FT SIGNAL 1 29
 FT CHAIN 30 425
 FT DOMAIN 30 251
 FT TRANSSEM 252 273
 FT DOMAIN 274 425
 FT DOMAIN 32 190
 FT REPEAT 32 66
 FT REPEAT 67 108
 FT REPEAT 109 148
 FT REPEAT 149 190
 FT REPEAT 198 249
 FT DOMAIN 354 419
 FT DISULFID 33 44
 FT DISULFID 45 58
 FT DISULFID 48 65
 FT DISULFID 68 84
 FT DISULFID 87 100
 FT DISULFID 90 108
 FT DISULFID 110 123
 FT DISULFID 126 139
 FT DISULFID 129 147
 FT DISULFID 150 165
 FT DISULFID 168 181
 FT DISULFID 171 189
 FT DISULFID 61 61
 FT CARBOHYD 71 71
 FT SEQUENCE 425 AA; 45432 MW; 7D78F258 CRC32;

Query Match 7.28; Score 207; DB 6; Length 425;
 Best Local Similarity 33.3%; Pred. No. 2,85e-20;
 Matches 43; Conservative 21; Mismatches 60; Indels 5; Gaps 4;

DB 45 ckaclnlgvayqpgan-gtycepcldsvtfsdvsatepckpcte-clglqsmasapve 102
 QY 41 CDKCPGGTYLKQHCATKATYCAPCPDH-YTDSWHTSDCLYCSVCKELQVYKQECNR 99
 DB 103 addavrcaygygdeetgtrceacvcsqglvifscqdkgnlycecpdgtydsdeanhv 162
 QY 100 THNRVCECKEGRYLEIE-FCLKHSRCPGGVQAGTPERNIVCKRCPDGFNSMSSK 157
 DB 163 dpcldpctvc 171
 QY 158 APCRKHNC 166

RESULT 15
 ID FASA BOVIN STANDARD: PRT: 323 AA.
 AC P51867;
 01-OCT-1996 (REL. 34, CREATED)
 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 FAST RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
 DE (APO-1 ANTIGEN) (CD95).
 GN APT1 OR FAS.
 OS BOS TAURUS (BOVINE).
 OS EURARCTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; ARTIODACTYLA.
 CC [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 96226401.
 RX YOO J., STONE R.T., BEATTIE C.W.;
 RL DNA CELL BIOC. 15:227-234(1996).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. MEDIATES
 CC -1- CELL DEATH. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE

CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
 CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR APOPTOSIS; RECEPTOR; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
 KW APOPTOSIS; RECEPTOR; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
 FT CHAIN 1 16
 FT SIGNAL 1 16
 FT DOMAIN 17 323
 FT TRANSMEM 171 188
 FT DOMAIN 189 323
 FT DOMAIN 45 163
 FT REPEAT 45 80
 FT REPEAT 81 124
 FT REPEAT 125 163
 FT DOMAIN 222 302
 SQ SEQUENCE 323 AA; 36445 MW; DA5A2A59 CRC32;

Query Match 6.6%; Score 188; DB 3; Length 323;
 St. Local Similarity 35.7%; Pred. No. 1.51e-16;
 Matches 40; Conservative 17; Mismatches 49; Indels 6; Gaps 6;
 Db 53 hqfcgpcpypgkxngdckrkgdtpcevicseagneytdkshskclrcs-icdeehgyle 111
 QY 37 HQLCDKCPETYLKQHOTAKMTV-CAPCPD-HYIDSMHTSDCLXSPVCKELQ-Y- 92
 Db 112 vegncltrntkrccksnfncsspcchncpctcehngilekctptcntkck 163
 QY 93 VKQECNRTNHRVCECKEGRYLIEFCLKHRSCP-GFGVQAGTPERNYVCK 143

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